

Wang 305217

1809

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/884,073

DATE: 12/17/97
TIME: 10:55:35

INPUT SET: S22123.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#4
ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: Hawkins, Phillip R.
6 Murry, Lynn E.
7
8 (ii) TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
9 METALLOPROTEINASES
10
11 (iii) NUMBER OF SEQUENCES: 5
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
15 (B) STREET: 3174 Porter Drive
16 (C) CITY: Palo Alto
17 (D) STATE: CA
18 (E) COUNTRY: US
19 (F) ZIP: 94304
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Diskette
23 (B) COMPUTER: IBM Compatible
24 (C) OPERATING SYSTEM: DOS
25 (D) SOFTWARE: FastSEQ Version 1.5
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: 08/884,073
29 (B) FILING DATE: 27-JUN-1997
30 (C) CLASSIFICATION: 514
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 08/588,163
34 (B) FILING DATE: 18-JAN-1996
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Luther, Barbara J.
38 (B) REGISTRATION NUMBER: 33,954
39 (C) REFERENCE/DOCKET NUMBER: PF-0053
40
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: 415-855-0555
43 (B) TELEFAX: 415-852-0195
44 (C) TELEX:
45
46

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/884,073DATE: 12/17/97
TIME: 10:55:40

INPUT SET: S22123.raw

47 (2) INFORMATION FOR SEQ ID NO:1:

48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 675 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

54

55 (ii) MOLECULE TYPE: cDNA

56

57 (vii) IMMEDIATE SOURCE:

58 (A) LIBRARY: METALLOPROTEINASES

59 (B) CLONE: 589345

60

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

62

63	ATGCCTGGGA	GCCCTCGGCC	CGCGCCAAGC	TGGGTGCTGT	TGCTGCGGCT	GCTGGCGTTG	60
64	CTGCGGCCCC	CGGGGCTGGG	TGAGGCATGC	AGCTGCGCCC	CGGCGCACCC	TCAGCAGCAC	120
65	ATCTGCCACT	CGGCAC TTGT	GATTCGGGCC	AAAATCTCCA	GTGAGAAGGT	AGTTCCGGCC	180
66	AGTGCAGACC	CTGCTGACAC	TGAAAAAATG	CTCCGGTATG	AAATCAAACA	GATAAAGATG	240
67	TTCAAAGGGT	TTGAGAAAGT	CAAGGATGTT	CAATATATCT	ATACGCCTTT	TGACTCTTCC	300
68	CTCTGTGGTG	TGAAACTAGA	AGCCAACAGC	CAGAAGCAGT	ATCTCTTGAC	TGGTCAGGTC	360
69	CTCAGTGATG	GAAAAGTCTT	CATCCATCTG	TGCAACTACA	TCGAGCCCTG	GGAGGACCTG	420
70	TCCTTGGTGC	AGAGGGAAAG	TCTGAATCAT	CACTACCATC	TGAACTGTGG	CTGCCAAATC	480
71	ACCACCTGCT	ACACAGTACC	CTGTACCATC	TCGGCCCCCTA	ACGAGTGCCT	CTGGACAGAC	540
72	TGGCTGTTGG	AACGAAAGCT	CTATGGTTAC	CAGGCTCAGC	ATTATGTCTG	TATGAAGCAT	600
73	GTTGACGGCA	CCTGCAGCTG	GTACCGGGGC	CACCTGCCTC	TCAGGAAGGA	GTTTGTTGAC	660
74	ATCGTTCAGC	CCTAG					675

75

76

77 (2) INFORMATION FOR SEQ ID NO:2:

78

79 (i) SEQUENCE CHARACTERISTICS:

80 (A) LENGTH: 224 amino acids

81 (B) TYPE: amino acid

82 (C) STRANDEDNESS: single

83 (D) TOPOLOGY: linear

84

85 (ii) MOLECULE TYPE: peptide

86

87 (vii) IMMEDIATE SOURCE:

88 (A) LIBRARY: METALLOPROTEINASES

89 (B) CLONE: 589345

90

91

92 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

93

94	Met	Pro	Gly	Ser	Pro	Arg	Pro	Ala	Pro	Ser	Trp	Val	Leu	Leu	Leu	Arg
95	1				5					10					15	
96	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Pro	Gly	Leu	Gly	Glu	Ala	Cys	Ser	Cys
97				20					25					30		
98	Ala	Pro	Ala	His	Pro	Gln	Gln	His	Ile	Cys	His	Ser	Ala	Leu	Val	Ile
99				35				40						45		

RAW SEQUENCE LISTING PATENT APPLICATION US/08/884,073

DATE: 12/17/97
TIME: 10:55:45

INPUT SET: S22123.raw

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100 Arg Ala Lys Ile Ser Ser Glu Lys Val Val Pro Ala Ser Ala Asp Pro
101      50      55      60
102 Ala Asp Thr Glu Lys Met Leu Arg Tyr Glu Ile Lys Gln Ile Lys Met
103      65      70      75      80
104 Phe Lys Gly Phe Glu Lys Val Lys Asp Val Gln Tyr Ile Tyr Thr Pro
105      85      90      95
106 Phe Asp Ser Ser Leu Cys Gly Val Lys Leu Glu Ala Asn Ser Gln Lys
107      100      105      110
108 Gln Tyr Leu Leu Thr Gly Gln Val Leu Ser Asp Gly Lys Val Phe Ile
109      115      120      125
110 His Leu Cys Asn Tyr Ile Glu Pro Trp Glu Asp Leu Ser Leu Val Gln
111      130      135      140
112 Arg Glu Ser Leu Asn His His Tyr His Leu Asn Cys Gly Cys Gln Ile
113      145      150      155      160
114 Thr Thr Cys Tyr Thr Val Pro Cys Thr Ile Ser Ala Pro Asn Glu Cys
115      165      170      175
116 Leu Trp Thr Asp Trp Leu Leu Glu Arg Lys Leu Tyr Gly Tyr Gln Ala
117      180      185      190
118 Gln His Tyr Val Cys Met Lys His Val Asp Gly Thr Cys Ser Trp Tyr
119      195      200      205
120 Arg Gly His Leu Pro Leu Arg Lys Glu Phe Val Asp Ile Val Gln Pro
121      210      215      220
122
123

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: METALLOPROTEINASES
- (B) CLONE: TIMP-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

141 Met Gly Ala Ala Ala Arg Thr Leu Arg Leu Ala Leu Gly Leu Leu Leu
142      1      5      10      15
143 Leu Ala Thr Leu Leu Arg Pro Ala Asp Ala Cys Ser Cys Ser Pro Val
144      20      25      30
145 His Pro Gln Gln Ala Phe Cys Asn Ala Asp Val Val Ile Arg Ala Lys
146      35      40      45
147 Ala Val Ser Glu Lys Glu Val Asp Ser Gly Asn Asp Ile Tyr Gly Asn
148      50      55      60
149 Pro Ile Lys Arg Ile Gln Tyr Glu Ile Lys Gln Ile Lys Met Phe Lys
150      65      70      75      80
151 Gly Pro Glu Lys Asp Ile Glu Phe Ile Tyr Thr Ala Pro Ser Ser Ala
152      85      90      95

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/884,073

DATE: 12/17/97
TIME: 10:55:51

INPUT SET: S22123.raw

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153 Val Cys Gly Val Ser Leu Asp Val Gly Gly Lys Lys Glu Tyr Leu Ile
154      100      105      110
155 Ala Gly Lys Ala Glu Gly Asp Gly Lys Met His Ile Thr Leu Cys Asp
156      115      120      125
157 Phe Ile Val Pro Trp Asp Thr Leu Ser Thr Thr Gln Lys Lys Ser Leu
158      130      135      140
159 Asn His Arg Tyr Gln Met Gly Cys Glu Cys Lys Ile Thr Arg Cys Pro
160      145      150      155      160
161 Met Ile Pro Cys Tyr Ile Ser Ser Pro Asp Glu Cys Leu Trp Met Asp
162      165      170      175
163 Trp Val Thr Glu Lys Asn Ile Asn Gly His Gln Ala Lys Phe Phe Ala
164      180      185      190
165 Cys Ile Lys Arg Ser Asp Gly Ser Cys Ala Trp Tyr Arg Gly Ala Ala
166      195      200      205
167 Pro Pro Lys Gln Glu Phe Leu Asp Ile Glu Asp Pro
168      210      215      220
169
170

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: METALLOPROTEINASES
- (B) CLONE: TIMP-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

188 Met Thr Pro Trp Leu Gly Leu Ile Val Leu Leu Gly Ser Trp Ser Leu
189      1      5      10      15
190 Gly Asp Trp Gly Ala Glu Ala Cys Thr Cys Ser Pro Ser His Pro Gln
191      20      25      30
192 Asp Ala Phe Cys Asn Ser Asp Ile Val Ile Arg Ala Lys Val Val Gly
193      35      40      45
194 Lys Lys Leu Val Lys Glu Gly Pro Phe Gly Thr Leu Val Tyr Thr Ile
195      50      55      60
196 Lys Gln Met Lys Met Tyr Arg Gly Phe Thr Lys Met Pro His Val Gln
197      65      70      75      80
198 Tyr Ile His Thr Glu Ala Ser Glu Ser Leu Cys Gly Leu Lys Leu Glu
199      85      90      95
200 Val Asn Lys Tyr Gln Tyr Leu Leu Thr Gly Arg Val Tyr Asp Gly Lys
201      100      105      110
202 Met Tyr Thr Gly Leu Cys Asn Phe Val Glu Arg Trp Asp Gln Leu Thr
203      115      120      125
204 Leu Ser Gln Arg Lys Gly Leu Asn Tyr Arg Tyr His Leu Gly Cys Asn
205      130      135      140

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/884,073

DATE: 12/17/97
TIME: 10:55:56

INPUT SET: S22123.raw

```

206   Cys Lys Ile Lys Ser Cys Tyr Tyr Leu Pro Cys Phe Val Thr Ser Lys
207   145                               150           155           160
208   Asn Glu Cys Leu Trp Thr Asp Met Leu Ser Asn Phe Gly Tyr Pro Gly
209                               165           170           175
210   Tyr Gln Ser Lys His Tyr Ala Cys Ile Arg Gln Lys Gly Gly Tyr Cys
211                               180           185           190
212   Ser Trp Tyr Arg Gly Trp Ala Pro Pro Asp Lys Ser Ile Ile Asn Ala
213                               195           200           205
214   Thr Asp Pro
215   210
216
217

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: METALLOPROTEINASES
- (B) CLONE: TIMP-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

233
234   Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
235   1           5           10           15
236   Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
237           20           25           30
238   Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
239           35           40           45
240   Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
241   50           55           60
242   Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
243   65           70           75           80
244   Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
245           85           90           95
246   His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
247           100          105          110
248   Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
249           115          120          125
250   Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
251   130          135          140
252   Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Ile Pro Cys
253   145          150          155          160
254   Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
255           165          170          175
256   Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
257           180          185          190
258   Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala

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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/884,073

DATE: 12/17/97
TIME: 10:56:01

INPUT SET: S22123.raw

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Original Text